

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCCATGAAGGAGTATGTG
CTCCTATTATTCTCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTTCCA
TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTACAGAGTTGTACATTGCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT
CTGATCCTGAACAACAACAAGCTAACGAAGATTCACCCAAAAGCCTTTCTAACCACAAAGAA
GTTGCGAAGGCTGTATCTGTCCCAATCAACTAAGTGAAATACCACTTAATCTTCCCAAAT
CATTAGCAGAACTCAGAATTGATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAA
GGAATGAATGCTTTACACGTTTTGGAATGAGTGCAAACCCTCTTGATAATAATGGGATAGA
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGCAGAAGCAAACTGACCT
CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACCTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT
TGGAACAATAAACTAAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG
AAATGCAACCTGCAACATTTGCTTGTGTTTTGAGCAGAATGAGTGTTGAGCTTGGGAACTTT
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT
TGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT
GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTGCGTACAAATGAT
CTTACATAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAAGTAAGATATTCGGTA
TTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT
TAGCAAAATTTGTGCTCTTTCATTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTTAAT
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT
CTTTATGTTTAAAACTAATTTCTTAAAAATAAAGCCTTCAGTAAATGTTTATTACCAACTTGA
TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATTATT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACCTCGCATTTT
AATGATCCGCTATTATAAGCTTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC
TTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGA
CACTAACAATTCTACACCAAATTTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAAATCAGAAA
ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

0944554 "083101

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKKLRRLLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNKKITDIENGLANIPRVREIHLENNKLKKIPSGLP
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

09041834.083101
TGTG20" 4834660

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCCGSCACCGCCCCCGGCCCGGCCCTCCGCCCTCCGCACTCGCGCCTCC
CTCCCTCCGCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCCCAGCTGTCCCGTTCGCGCTCATGCCGAGCCTCCC
GGCCCCCGCGGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGGCCCGCGGCGCCGGCCAGA
GCCCCCGTGTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTCGGGGAGCGGCAGGCTGCACCTTCGGCGG
GAAGGTCTATGCCCTTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTTCGGGGTGATGCGCTGCGTGCTGTG
CGCCTGCGAGGCGCCTCAGTGGGGTCCGCGTACCAGGGGCCCTGGCAGGGTCACTGCAAGAACATCAAACCAGA
GTGCCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGCCAGACCTGCCCCAGGAGCGCAG
CAGTTCGAGCGGCAGCCGAGCGGCCTGTCTTTCAGTATCCGCGGGACCCGGAGCATCGCAGTTATAGCGACCG
CGGGGAGCCAGGCGCTGAGGAGCGGGCCCCGTGGTGACGGCCACACGGAATTTCGTGGCGCTGCTGACAGGGCCGAG
GTCGCAGGCGGTGGCACGAGCCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCT
GGACCGCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGGAGCACCTGCAGCCCCACCCA
AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA
TGTGGCACTTGTGACACTCACTCACCTTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGGCTGC
AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCCACAGCAGGGCGTAGGGGGCATCACCTGCTCACTCT
CAGTGACACAGAGGACTCCTTGCATTTTTTGCTGCTCTTCCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCA
GGAACCAAGGCTTGTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGGTGGGGGAGTGCAG
GATGGCCCTGGAGTGGGCAGGCGAGGCTGCGCATCAGTGGAGACACATTGCTGCCAGGAAGAGCTGCGAGCT
CCTGCAAAGTGTCTTTTGTGGGGCTGATGCCCTGATCCAGTCCAGACGGGTGCTGCCGGCTCAGCCAGCCTCAC
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGACACT
GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCTGTGCCACATGGCTGGACTCCAGCCAGGAGGACACAC
GGCGTGGGTATCTGCCCTGGGCTGGGTGCCGAGGGGCTCATATGCTGCTGCAGAATGAGCTCTTCTGAACGT
GGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGACGTTGGCTGCCCTGCCCTACTGTGGGCATAGCGCCCG
CCATGACACGCTGCCCGTGCCCTAGCAGGAGCCCTGGTGCTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC
CTGGCTTTCTTGGATACCCACTGTCACTGTCACTATGAAGTGTGCTGGCTGGGCTTGGTGGCTCAGAACAAGG
CACTGTCACTGCCCACCTCCTTGGGCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTC
AGAGGCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCGGCACCTGGCAAAGGCATGGCCTCCCTGAT
GATCACCAACCAAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATAGCCAACCAATGTGAGGTTGGCGG
ACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCC
TGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCTGGGCGGCCCGAGACCCCAACACATG
CTTCTTCGAGGGGAGCAGCGCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCAC
CTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCGCCAGCTGCCACACCCGGTGCAGGCTCC
CGACCAAGTGCTGCCCTGTTTGCCTGAGAAACAAGATGTGAGAGCTTGCCAGGGCTGCCAAGGAGCCGGGACCC
AGGAGAGGGCTGCTATTTTGTGAGTGTGCTGTGACCTGCAAGGGGGGCACTGGAGAGGTGCATGTGAGAAGGTGCA
TCCCCGGCTGGCCTGTGCCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGTGGGGTGGG
GGCCACCCCGAGCTGGGGGACCCCATGCAAGGCTGATGGGCCCCGGGGCTGCCGTTTTGTGCTGGGCAGTGGTTCCC
AGAGAGTCAGAGCTGGCACCCCTCAGTGGCCCCCTTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGCAGG
GGTGCCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTGCATGCTGTTC
CCGCTGCACGGCCACCGGCGGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTA
GGGAGCAGCCAGAGGGCCAAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT
GCATTCTCCTGTGGGAAGCCCAGTGCCCTTGTCTCTGTCTGCTCTACTCCCACCCCACTACCTCTGGGAA
CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCTGCCCTGCCACCC
TCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTA
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
TTTTGTATTTATTAACCATTTCTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

094434-0340

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHPDLGQPFQVMRCVLCACEAPQWGRRTGRVSCVNIKPECPTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAEERARGDGHTDFVALLTGPRSQAVAR
ARVSLLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGLLRELQANVSAQEPGFAEVLNLTQVQEMD
WLVLGELQMALEWAGRPGRLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAAML
LQNELFLNVGTKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRLLKGFYGYSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGLRLEAAGAEGVRALGAPDTASAAPPVV
PGLPALAPAKPGGPGRPRDPNTCFEQQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC
PPSCPHPVQAPDQCCPVCPEKQDVRDLPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPF
GLIKCAVCTCKGGTGEVHCEKVQCPLACAQPVVNPTDCCKQCPVGS GAHPQLGDPMQADG
PRGCRFAGQWFPESQSWHPSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

0944034.003104

FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCCGTCCTGCG
TCCTGGCTCCGGCTCCCGGCCCTCCCGGCCGCCATGCAGCCCCGCCGCCAGGCGCCCGGTGCGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG
CCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG
AGCCGACCCGAGCACC CGGCCCGCCGCCGCGAGCCTGGCTACAGCTGCACCTGCCCCGCCGGGATCTCCGGCG
CCAATGCCAGCTTGTTCAGATCCTTGTGCCAGCAACCCTTGTACCATTGGCAACTGCAGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTGTGAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACCTCCAGTC
TCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTTCTGCTACTCAGGAGCCTGACA
AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCCTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTCGGCAAGATGCCACTGCCCTCACTGATTTTGC
TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT
CAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG
TGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACG
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTCTCTGACCTGTG
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACGCGAGCT
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCTGGTTATACCTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT
GCCAGAACAACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA
CCTGTGCCCAGCTTATTGACTTCTGTGCCCTCAGCCCCGTGTGCTCATGGCACGTGCCGAGCGTGGGCACCAGCT
ACAAATGCCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCTGGCAGAATACAAAGGAACAC
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCAGCTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA
ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCACATTGACATAAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGGAGCTGCCTGGACCAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG
CAAATGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC
TCTACATCATCATTTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTGTCCGCA
TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACTGCCGCAGCATCGACAGCG
AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAGAAAATCCCGGCCGTGCAATGTATGATGTGA
GCCCCATCGCCTATGAAGATTACAGTCTGATGACAAACCCTTGGTCACACTGATTAAAACTAAAGATTTGTAAAT
CTTTTTTTGGATTATTTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTTAAGAAAATAAAAAGCTTAA
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTAGTAGAATATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG
GAAAAATATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAACTGT
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAATTTCTGTGGTTGTTACA
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGAGTGCCGGCTTTCTGAGTAGAGTTAGGAAAACCAC
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTTCGTTTTGTGAAA
AGAAACTAGTTAAATTTACTATTCTTAACCCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAGTAAC
TTATTTCTGCAGTGTTTTGTGAACTTTGTGGAAACATTCTTTCAGTTTGTGTTTTGTGCTATTTTCGTAACAGTCG
TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCGATTGATTTGAATCTATATTT
TTCTTTAAAAAGTCAAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTTTCTTCACTAGTGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGTATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
AAGTCA

094404-03101

00000000000000000000000000000000

><MW: 78475, pI: 5.09, NX(S/T): 11

Signal sequence.

Transmembrane domain.

N-glycosylation sites.

Glycosaminoglycan attachment site.

Tyrosine kinase phosphorylation sites.

N-myristoylation sites.

Amidation site.

Aspartic acid and asparagine hydroxylation site.

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

09044834.083101

FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTA
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

107280-128456

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAACAAATGGC
AAAGCCCCCTTGGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCTTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGCAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCAGTGTAGCAAGCCACAGACACCCACAAAGTTCCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

0954484.083101

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQAALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSKALND
TQKLACLIQVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

034434 083101
T01E80 10314650

FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC
AACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCCCTGGAG
CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCGCTACCTGACGCTC
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTCACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCCTTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCTTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGA
ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACC

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FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT

094484-083101
TOTEDD-4884660

FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC
CTGCGCCACCGCCGCGCGAGCCGAGCCCGCCGCGCGCCCCCGGAGCGCCGGCCCCATGCCC
GCCGGCCGCGGGGGCCCCGCGCCCAATCCGCGCGGCGGCCGCGCCGCTTGCTGCCCCCTGCT
GCTGCTGCTCTGCGTCCTCGGGGCGCCGCGAGCCGGATCAGGAGCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA
GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAACGGGCGCCGCTGCCCCC
TGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGT
CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCCGTGACGGCAGCATCCTGGCTGGC
TCCTGCCTCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCCACGGGGAGACCTTCCTCCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAG
GACCAGCTGAGCGTGCGCTGGGTGTGCGCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC
TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCTCCACTCCCCGAGTGAGCGCCCGGGCCCCGGGCGGCGGGGCGTGCGAACCGC
GGGGCGGAGAGCCGAGCTCGGGGCCGTGCGGCGCGAGCTCAAGCAGTTCTTGGGCTGGCTC
AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGAT
GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA
CGGCGAGAGGTCCTGCCAGATAAGCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGA
CGCAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGGTGGCCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT
GAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTGAAAAAAAAA
AAA

0994484-083101

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQSRGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSCLKYKLRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIVWEATNRLGSARSDVLTLDILDVVTDDPPPDVHVS RVGG
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

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101E80-48844650

09-1867-0831

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDSCNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

5944834.083404
TQFESQ"4884855

FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCAACAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGGCGTCCGGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC
TGCTCCTGGGCCTGGCGGGCCGGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGGTGCTCTCTTCTGGTCCTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAA
AAAAAAAAAAAAA

09944884, 083101

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

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FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGACAGGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCA
GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTAAAGACCACATGCCTCATGTCAAAGAGGTCTCAGA
CCTTGACAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

09944384 "083101

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSDSLAAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPPG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPGS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

09944864.083101

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCGCCATGCTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCCTTCACTACGGTTTCTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAGGAATAAAACCAACAGAGAAGAAAATGGAGAGAAGGGGACTGAAATATTCAG
AGCTTCTGCAGTGATTCCAGCAAGGACAAAGCCGCCTTTTTCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGGCACTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCAT
CTACTGTCAATTAACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA
AAGACCTTCTCCTTTACCCAAGAATGTGGTATTTCGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCCA
GGACCGTTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGACATTACCATATGTCAACCACTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCCAAGG
TCGGGGAGAGCGCACACCCTCAAGATCCTCAACAACACCCGAGAGGCGCGCCGAGGCCAAGTC
TGCATCTTCAACATTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTCGCT
GGAGAACTGTGGCCTCACACGGCGCGTGCACGAGGAGGAGGACGAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTCACCGCCAGCAACA
GTAAGAAATTATCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCTGGAGGCGATGGAGAGGGGGACACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG
CATGTGCGGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGAGGAGCTGGCACGCAGC
CAGGACCTTTGCTCAAGAAGCCAACTCCGTCAAAAAAAAAACAAAACAAAACAAAAAAGA
CATGGGAGAGATGGTGTTTTTCTCTCCACCACCTGGGGATACGATTGAGAAAGATGGCCACCT
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAAATGTGTTTTGTTTAAGCTAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTTEENGEKGTETIFRASAVIPSKDKAAFFLSYEELLQRRLLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVKDHLISVTPDSIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKI LNNTREAARGQVCIF
TIGIGNDVDVFRLLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVDRLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTG
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

0944934.083101

FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCTAGCTACTGAA
TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTTAGATCAGCCTTTTTGTTTCAAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

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FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAAAAPPGLRLLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQMLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPMVMTWVRVDDEMPQHAVLSGPNLFINNLNKT DNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTILTIIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

03944584.033101

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCCGA
CCCCCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCGCCGCCTC
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
GGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
GCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA
GCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCCGGCATCCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCCAGCTGCGGGCC
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACA
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCCGCCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACACAGCCACAGTGCCCAACA
CGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
CCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG
GGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGC
CAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTACGCCGAGGGCCACCACGGTCCCT
GACCTTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG
GCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCCGGGCGGGTGCCGGAGGGCG
AGGAGGCCTGCGGGGAGGGCCATACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
CAGGCCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGC
CGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGGCCCCTGGAACCTGGAGGGAGTGAAGGTC
CCCTTGGAGCCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGC
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCATATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGGCCCTGCCATGTGCTGGTAAC
GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTTGTCTTTTAA
AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACCTC
AGAGACAAGGACTTTGGTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAA
ATAAAAAAAAAA

094484-083101

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N
G I T M L D A S S F A G L P G L Q L L D L S Q N Q I A S L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E A L R L
A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L A
G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P
E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P
A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q
G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V
T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E
G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P
G P K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

09944804 083401

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCCTACCCTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCCCTCCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTTCCCATTAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTCACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCATAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAAACTGTGATT
GTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGGTTTGGCTC
CCCGTTCCTCACTTTTCCCTTTTCATTCCCACCCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

0994484-083101

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFL LAPKGPPGNMG GPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQH SVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVII PRARAKLNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

0994484-033101

FIGURE 29

CACTTTCTCCCTCTCTTCCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCCGGCAGGAAGATGGGC
TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCTTTGCTCTGGCCTGGT
CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC
GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCGGCAAGTTCTACTGCTAC
GTGCCCGGCTCTACTTCTTTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC
CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC
GAGACGCGGGTGGCGGCAGGGCGTCCAGGGTGCGGCACCGCGGCTCCAGTCCTTGGAATA
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAAGGGAGGGGCCGGGGCAGG
AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACTTTCTTGAGGGATAGGTGGACC
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT
GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCCCTGGCATCGGCT
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCCTTGGCTTCTGTTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT
CATCCAGGCCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATTCAGTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCC
ATAGCCCCCTCTCCACCTCACCCCATGTTGATGCCCAGGGTCACTCTTGCTACCCGCTGGGCC
CCCAAACCCCCGCTGCCTCTCTTCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC
TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
CTGCGGGTCACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

09944884-083101

FIGURE 31

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCCGCGCGGATTGCGCCGGTCCTTCCCGCGG
GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAAGAGGGAGGATTAT
CCTTGACCTTTGAAGACCAAACCTAACTGAAATTTAAAATGTTCTTTCGGGGGAGAAGGGAG
CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC
AAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
GACAACCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA
CATAACACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
AGCCTCCCACGACCCTCATTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATAACGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCTA
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGTTGATAGGCC
TCGTCCTCCTGGGTAGAATCCTTTCCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
TAGTAACCAGAAGCCCAAATGCAATGAGTTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTG
TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
CCACACCTGGGTGATTTTTGTATTTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG
GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC
TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTTAAACTTATT
CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

099484-03101

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

09941984-083104
T07E90-498460

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAAGTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

0904184-083104

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTDGSTRLNNDKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCI PKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

09044834 083104
TOTESD 483460